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Response Under 37 CFR §1.116
Expedited Procedure
Examining Group 1644

CASE 4-31336P1

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IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

IN RE APPLICATION OF
CROWL ET AL.
APPLICATION NO: 09/522,699
FILED: MARCH 10, 2000
FOR: ARTHRITIS-ASSOCIATED PROTEIN

Art Unit: 1644
Examiner: P. Nolan

Box AF
Assistant Commissioner for Patents
Washington, D.C. 20231

AMENDMENT AFTER FINAL REJECTION

Sir:

This communication is in response to the final Office Action mailed on October 2, 2002.

Applicants gratefully acknowledge the Examiner's allowance of claims 1, 2, 7, 10, 11, 20, and 21.

Applicants respectfully request reconsideration of the Examiner's rejection of claims 3, 4, 9, and 22 for lack of written description. In particular, the Examiner asserted that:

> Applicant has no written support in the originally filed claims for a polynucleotide comprising at least 297 contiguous nucleotides of coding sequence.
>
> Applicant has support for a single polynucleotide fragment that is 297 nucleotides long but not for a genus of polynucleotide fragments that are at least 297 contiguous nucleotides of coding sequence long.

Applicant respectfully submits that the description of the genus set forth in claim 3 need not be found in the originally filed claims, but can be (and is) also present in the specification as originally filed. Thus, applicant respectfully points out the following.

Example 2 (starting on page 25 of the present specification) describes the assembly of an expression construct for the adlican protein. On page 25, line 10, a lambda gt11 clone that contains nucleotides 1 to 715 of the coding region of SEQ ID NO:1 is set out. Lines 23 to 25 describe clone E3 which contains 3969 nucleotides of coding sequence. Lines 26 to 28 describe a 778 nucleotide fragment of coding sequence from SEQ ID NO:1. The ligated product of the 778 nucleotide fragment and the 3969 nucleotide fragment, referred to at line 30 of page 25 to line 1 of page 26, is a 4427 nucleotide fragment of the coding sequence from SEQ ID NO:1. The ligation described at lines 1 to 5 of page 26 makes a 4446 nucleotide fragment of the coding sequence of SEQ ID NO:1.

Lines 6 to 8 describe the generation of a 320 nucleotide fragment of the coding sequence of SEQ ID NO:1, and lines 8 to 9 describe the generation of a 297 nucleotide fragment of the coding sequence of SEQ ID NO:1. Lines 9 to 10 describes the generation of a 2707 nucleotide fragment of the coding sequence of SEQ ID NO:1, and lines 10 to 13 describe the generation of a 3325 nucleotide fragment of the coding sequence of SEQ ID NO:1. Lines 14 to 17 describe the generation of a 4040 nucleotide fragment of the coding sequence of SEQ ID NO:1, and lines 18 to 23 describe the generation of the full length coding region of SEQ ID NO:1.

Thus, Example 2 describes nucleotide fragments of the coding sequence of SEQ ID NO:1 of 297 nucleotides, 320 nucleotides, 715 nucleotides, 778 nucleotides, 2702 nucleotides, 3325 nucleotides, 3969 nucleotides, 4040 nucleotides, 4427 nucleotides, 4446 nucleotides, and the full coding sequence from SEQ ID NO:1. Eleven fragments within the scope of the "...polynucleotide comprising at least 297 contiguous nucleotides of coding sequence from SEQ ID NO:1" feature of claim 3 are specifically described by Example 2.

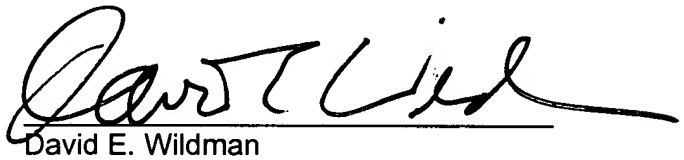
It is respectfully submitted that applicants have described a representative number of species within the scope of the genus of claim 3 and those claims dependent therefrom to support the written description of claim 3. Present claim 3 is narrower than claim 3 as originally filed. With respect to the scope of the recited genus of polynucleotides, which starts at 297 nucleotides of coding sequence and goes up to the full coding sequence, it is respectfully submitted that the disclosure of, *inter alia*, Example 2 fully supports this scope.

The facts are analogous to those of *In re Wertheim*, 541 F.2d 257, 191 USPQ 90 (C.C.P.A. 1976) where an initial range of 25 to 60% solids content was disclosed, along with examples of 36 and 50% solids content. A claim of between 35 and 60% solids was held to be described adequately (note the decrease in scope from the 25% range initially disclosed up to 35% as the lower end of the solids range). It is submitted that the same situation obtains here. Claim 3 initially

claimed a vector comprising any size fragment of the isolated DNA of claim 1 (i.e., a DNA comprising SEQ ID NO:1). Applicants have narrowed the scope of the vectors of claim 3 by increasing the minimum size of the coding sequence nucleotide fragment to 297 nucleotides, an embodiment specifically set out in the specification. Ten other fragments of varying representative sizes, ranging up all the way to the full length coding sequence, are also specifically disclosed. Thus, it is respectfully submitted that applicants' specification clearly reasonably describes what is claimed to one of ordinary skill in the art, and the rejection under 35 U.S.C. § 112, first paragraph, for lack of written description, should be withdrawn.

If, in light of the above remarks, the Examiner does not consider all of the pending claims to be in condition for allowance, applicants respectfully request an interview with the Examiner, and request that the Examiner contact the undersigned at the telephone number set out below.

Respectfully submitted,



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